

#8  
Dmt  
1-31-02RECEIVED  
JAN 30 2002  
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1646

## RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/09/647,544

TIME: 14:51:51

Input Set : A:\003300-685.ST25.txt

Output Set: N:\CRF3\01222002\I647544.raw

PS

ENTERED

```

4 <110> APPLICANT: Lundgren-Akerlund, Evy
6 <120> TITLE OF INVENTION: Integrin Heterodimer and a Subunit Thereof
8 <130> FILE REFERENCE: 003300-685
10 <140> CURRENT APPLICATION NUMBER: US 09/647,544
11 <141> CURRENT FILING DATE: 2000-10-26
13 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00544
14 <151> PRIOR FILING DATE: 1999-03-31
16 <150> PRIOR APPLICATION NUMBER: SE 9801164-6
17 <151> PRIOR FILING DATE: 1998-04-02
19 <150> PRIOR APPLICATION NUMBER: SE 9900319.6
20 <151> PRIOR FILING DATE: 1999-01-28
22 <160> NUMBER OF SEQ ID NOS: 21
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3884
28 <212> TYPE: DNA
29 <213> ORGANISM: Human
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (22)...(3522)
35 <400> SEQUENCE: 1
36 caggtcagaa accgatcagg c atg gaa ctc ccc ttc gtc act cac ctg ttc 51
37 Met Glu Leu Pro Phe Val Thr His Leu Phe
38 1 5 10
40 ttg ccc ctg gtg ttc ctg aca ggt ctc tgc tcc ccc ttt aac ctg gat 99
41 Leu Pro Leu Val Phe Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp
42 15 20 25
44 gaa cat cac cca cgc cta ttc cca ggg cca cca gaa gct gaa ttt gga 147
45 Glu His His Pro Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly
46 30 35 40
48 tac agt gtc tta caa cat gtt ggg ggt gga cag cga tgg atg ctg gtg 195
49 Tyr Ser Val Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val
50 45 50 55
52 ggc gcc ccc tgg gat ggg cct tca ggc gac cgg agg ggg gac gtt tat 243
53 Gly Ala Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr
54 60 65 70
56 cgc tgc cct gta ggg ggg gcc cac aat gcc cca tgt gcc aag ggc cac 291
57 Arg Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
58 75 80 85 90
60 tta ggt gac tac caa ctg gga aat tca tct cat cct gct gtg aat atg 339
61 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn Met
62 95 100 105
64 cac ctg ggg atg tct ctg tta gag aca gat ggt gat ggg gga ttc atg 387

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65 His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly Phe Met  
 66 110 115 120  
 68 gcc tgt gcc cct ctc tgg tct cgt gct tgt ggc agc tct gtc ttc agt  
 69 Ala Cys Ala Pro Leu Trp Ser Arg Ala Cys Gly Ser Ser Val Phe Ser  
 70 125 130 135  
 72 tct ggg ata tgt gcc cgt gtg gat gct tca ttc cag cct cag gga agc 483  
 73 Ser Gly Ile Cys Ala Arg Val Asp Ala Ser Phe Gln Pro Gln Gly Ser  
 74 140 145 150  
 76 ctg gca ccc act gcc caa cgc tgc cca aca tac atg gat gtt gtc att 531  
 77 Leu Ala Pro Thr Ala Gln Arg Cys Pro Thr Tyr Met Asp Val Val Ile  
 78 155 160 165 170  
 80 gtc ttg gat ggc tcc aac agc atc tac ccc tgg tct gaa gtt cag acc 579  
 81 Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Ser Glu Val Gln Thr  
 82 175 180 185  
 84 ttc cta cga aga ctg gta ggg aaa ctg ttt att gac cca gaa cag ata 627  
 85 Phe Leu Arg Arg Leu Val Gly Lys Leu Phe Ile Asp Pro Glu Gln Ile  
 86 190 195 200  
 88 cag gtg gga ctg gta cag tat ggg gag agc cct gta cat gag tgg tcc 675  
 89 Gln Val Gly Leu Val Gln Tyr Gly Glu Ser Pro Val His Glu Trp Ser  
 90 205 210 215  
 92 ctg gga gat ttc cga acg aag gaa gaa gtg gtg aga gca gca aag aac 723  
 93 Leu Gly Asp Phe Arg Thr Lys Glu Glu Val Val Arg Ala Ala Lys Asn  
 94 220 225 230  
 96 ctc agt cgg cgg gag gga cga gaa aca aag act gcc caa gca ata atg 771  
 97 Leu Ser Arg Arg Glu Gly Arg Glu Thr Lys Thr Ala Gln Ala Ile Met  
 98 235 240 245 250  
 100 gtg gcc tgc aca gaa ggg ttc agt cag tcc cat ggg ggc cga ccc gag 819  
 101 Val Ala Cys Thr Glu Gly Phe Ser Gln Ser His Gly Gly Arg Pro Glu  
 102 255 260 265  
 104 gct gcc agg cta ctg gtg gtt gtc act gat gga gag tcc cat gat gga 867  
 105 Ala Ala Arg Leu Leu Val Val Val Thr Asp Gly Glu Ser His Asp Gly  
 106 270 275 280  
 108 gag gag ctt cct gca gca cta aag gcc tgt gag gct gga aga gtg aca 915  
 109 Glu Glu Leu Pro Ala Ala Leu Lys Ala Cys Glu Ala Gly Arg Val Thr  
 110 285 290 295  
 112 cgc tat ggg att gca gtc ctt ggt cac tac ctc cgg cgg cag cga gat 963  
 113 Arg Tyr Gly Ile Ala Val Leu Gly His Tyr Leu Arg Arg Gln Arg Asp  
 114 300 305 310  
 116 ccc agc tct ttc ctg aga gaa att aga act att gcc agt gat cca gat 1011  
 117 Pro Ser Ser Phe Leu Arg Glu Ile Arg Thr Ile Ala Ser Asp Pro Asp  
 118 315 320 325 330  
 120 gag cga ttc ttc ttc aat gtc aca gat gag gct gct ctg act gac att 1059  
 121 Glu Arg Phe Phe Phe Asn Val Thr Asp Glu Ala Ala Leu Thr Asp Ile  
 122 335 340 345  
 124 gtg gat gca cta gga gat cgg att ttt ggc ctt gaa ggg tcc cat gca 1107  
 125 Val Asp Ala Leu Gly Asp Arg Ile Phe Gly Leu Glu Gly Ser His Ala  
 126 350 355 360  
 128 gaa aac gaa agc tcc ttt ggg ctg gaa atg tct cag att ggt ttc tcc 1155  
 129 Glu Asn Glu Ser Ser Phe Gly Leu Glu Met Ser Gln Ile Gly Phe Ser

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130	365	370	375	
132	act cat cgg cta aag gat ggg att ctt ttt ggg atg gtg ggg gcc tat	1203		
133	Thr His Arg Leu Lys Asp Gly Ile Leu Phe Gly Met Val Gly Ala Tyr			
134	380 385 390			
136	gac tgg gga ggc tct gtg cta tgg ctt gaa gga ggc cac cgc ctt ttc	1251		
137	Asp Trp Gly Gly Ser Val Leu Trp Leu Glu Gly Gly His Arg Leu Phe			
138	395 400 405 410			
140	ccc cca cga atg gca ctg gaa gac gag ttc ccc cct gca ctg cag aac	1299		
141	Pro Pro Arg Met Ala Leu Glu Asp Glu Phe Pro Pro Ala Leu Gln Asn			
142	415 420 425			
144	cat gca gcc tac ctg ggt tac tct gtt tct tcc atg ctt ttg cgg ggt	1347		
145	His Ala Ala Tyr Leu Gly Tyr Ser Val Ser Ser Met Leu Leu Arg Gly			
146	430 435 440			
148	gga cgc cgc ctg ttt ctc tct ggg gct cct cga ttt aga cat cga gga	1395		
149	Gly Arg Arg Leu Phe Leu Ser Gly Ala Pro Arg Phe Arg His Arg Gly			
150	445 450 455			
152	aaa gtc atc gcc ttc cag ctt aag aaa gat ggg gct gtg agg gtt gcc	1443		
153	Lys Val Ile Ala Phe Gln Leu Lys Lys Asp Gly Ala Val Arg Val Ala			
154	460 465 470			
156	cag agc ctc cag ggg gag cag att ggt tca tac ttt ggc agt gag ctc	1491		
157	Gln Ser Leu Gln Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Glu Leu			
158	475 480 485 490			
160	tgc cca ttg gat aca gat agg gat gga aca act gat gtc tta ctt gtg	1539		
161	Cys Pro Leu Asp Thr Asp Arg Asp Gly Thr Thr Asp Val Leu Leu Val			
162	495 500 505			
164	gct gcc ccc atg ttc ctg gga ccc cag aac aag gaa aca gga cgt gtt	1587		
165	Ala Ala Pro Met Phe Leu Gly Pro Gln Asn Lys Glu Thr Gly Arg Val			
166	510 515 520			
168	tat gtg tat ctg gta ggc cag cag tcc ttg ctg acc ctc caa gga aca	1635		
169	Tyr Val Tyr Leu Val Gly Gln Gln Ser Leu Leu Thr Leu Gln Gly Thr			
170	525 530 535			
172	ctt cag cca gaa ccc ccc cag gat gct cgg ttt ggc ttt gcc atg gga	1683		
173	Leu Gln Pro Glu Pro Pro Gln Asp Ala Arg Phe Gly Phe Ala Met Gly			
174	540 545 550			
176	gct ctt cct gat ctg aac caa gat ggt ttt gct gat gtg gct gtg ggg	1731		
177	Ala Leu Pro Asp Leu Asn Gln Asp Gly Phe Ala Asp Val Ala Val Gly			
178	555 560 565 570			
180	gcg cct ctg gaa gat ggg cac cag gga gca ctg tac ctg tac cat gga	1779		
181	Ala Pro Leu Glu Asp Gly His Gln Gly Ala Leu Tyr Leu Tyr His Gly			
182	575 580 585			
184	acc cag agt gga gtc agg ccc cat cct gcc cag agg att gct gct gcc	1827		
185	Thr Gln Ser Gly Val Arg Pro His Pro Ala Gln Arg Ile Ala Ala Ala			
186	590 595 600			
188	tcc atg cca cat gcc ctc agc tac ttt ggc cga agt gtg gat ggt cgg	1875		
189	Ser Met Pro His Ala Leu Ser Tyr Phe Gly Arg Ser Val Asp Gly Arg			
190	605 610 615			
192	cta gat ctg gat gga gat gat ctg gtc gat gtg gct gtg ggt gcc cag	1923		
193	Leu Asp Leu Asp Gly Asp Asp Leu Val Asp Val Ala Val Gly Ala Gln			
194	620 625 630			

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196 ggg gca gcc atc ctg ctc agc tcc cgg ccc att gtc cat ctg acc cca 1971
197 Gly Ala Ala Ile Leu Leu Ser Ser Arg Pro Ile Val His Leu Thr Pro
198 635 640 645 650
200 tca ctg gag gtg acc cca cag gcc atc agt gtg gtt cag agg gac tgt 2019
201 Ser Leu Glu Val Thr Pro Gln Ala Ile Ser Val Val Gln Arg Asp Cys
202 655 660 665
204 agg cgg cga ggc caa gaa gca gtc tgt ctg act gca gcc ctt tgc ttc 2067
205 Arg Arg Arg Gly Gln Glu Ala Val Cys Leu Thr Ala Ala Leu Cys Phe
206 670 675 680
208 caa gtg acc tcc cgt act cct ggt cgc tgg gat cac caa ttc tac atg 2115
209 Gln Val Thr Ser Arg Thr Pro Gly Arg Trp Asp His Gln Phe Tyr Met
210 685 690 695
212 agg ttc acc gca tca ctg gat gaa tgg act gct ggg gca cgt gca gca 2163
213 Arg Phe Thr Ala Ser Leu Asp Glu Trp Thr Ala Gly Ala Arg Ala Ala
214 700 705 710
216 ttt gat ggc tct ggc cag agg ttg tcc cct cgg agg ctc cgg ctc agt 2211
217 Phe Asp Gly Ser Gly Gln Arg Leu Ser Pro Arg Arg Leu Arg Leu Ser
218 715 720 725 730
220 gtg ggg aat gtc act tgt gag cag cta cac ttc cat gtg ctg gat aca 2259
221 Val Gly Asn Val Thr Cys Glu Gln Leu His Phe His Val Leu Asp Thr
222 735 740 745
224 tca gat tac ctc cgg cca gtg gcc ttg act gtg acc ttt gcc ttg gac 2307
225 Ser Asp Tyr Leu Arg Pro Val Ala Leu Thr Val Thr Phe Ala Leu Asp
226 750 755 760
228 aat act aca aag cca ggg cct gtg ctg aat gag ggc tca ccc acc tct 2355
229 Asn Thr Thr Lys Pro Gly Pro Val Leu Asn Glu Gly Ser Pro Thr Ser
230 765 770 775
232 ata caa aag ctg gtc ccc ttc tca aag gat tgt ggc cct gac aat gaa 2403
233 Ile Gln Lys Leu Val Pro Phe Ser Lys Asp Cys Gly Pro Asp Asn Glu
234 780 785 790
236 tgt gtc aca gac ctg gtg ctt caa gtg aat atg gac atc aga ggc tcc 2451
237 Cys Val Thr Asp Leu Val Leu Gln Val Asn Met Asp Ile Arg Gly Ser
238 795 800 805 810
240 agg aag gcc cca ttt gtg gtt cga ggt ggc cgg cgg aaa gtg ctg gta 2499
241 Arg Lys Ala Pro Phe Val Val Arg Gly Gly Arg Arg Lys Val Leu Val
242 815 820 825
244 tct aca act ctg gag aac aga aag gaa aat gct tac aat acg agc ctg 2547
245 Ser Thr Thr Leu Glu Asn Arg Lys Glu Asn Ala Tyr Asn Thr Ser Leu
246 830 835 840
248 agt atc atc ttc tct aga aac ctc cac ctg gcc agt ctc act cct cag 2595
249 Ser Ile Ile Phe Ser Arg Asn Leu His Leu Ala Ser Leu Thr Pro Gln
250 845 850 855
252 aga gag agc cca ata aag gtg gaa tgt gcc gcc cct tct gct cat gcc 2643
253 Arg Glu Ser Pro Ile Lys Val Glu Cys Ala Ala Pro Ser Ala His Ala
254 860 865 870
256 cgg ctc tgc agt gtg ggg cat cct gtc ttc cag act gga gcc aag gtg 2691
257 Arg Leu Cys Ser Val Gly His Pro Val Phe Gln Thr Gly Ala Lys Val
258 875 880 885 890
260 acc ttt ctg cta gag ttt gag ttt agc tgc tcc tct ctc ctg agc cag 2739

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261 Thr Phe Leu Leu Glu Phe Glu Phe Ser Cys Ser Ser Leu Leu Ser Gln
262      895      900      905
264 gtc ttt ggg aag ctg act gcc agc agt gac agc ctg gag aga aat ggc 2787
265 Val Phe Gly Lys Leu Thr Ala Ser Ser Asp Ser Leu Glu Arg Asn Gly
266      910      915      920
268 acc ctt caa gaa aac aca gcc cag acc tca gcc tac atc caa tat gag 2835
269 Thr Leu Gln Glu Asn Thr Ala Gln Thr Ser Ala Tyr Ile Gln Tyr Glu
270      925      930      935
272 ccc cac ctc ctg ttc tct agt gag tct acc ctg cac cgc tat gag gtt 2883
273 Pro His Leu Leu Phe Ser Ser Glu Ser Thr Leu His Arg Tyr Glu Val
274      940      945      950
276 cac cca tat ggg acc ctc cca gtg ggt cct ggc cca gaa ttc aaa acc 2931
277 His Pro Tyr Gly Thr Leu Pro Val Gly Pro Gly Pro Glu Phe Lys Thr
278 955      960      965      970
280 act ctc agg gtt cag aac cta ggc tgc tat gtg gtc agt ggc ctc atc 2979
281 Thr Leu Arg Val Gln Asn Leu Gly Cys Tyr Val Val Ser Gly Leu Ile
282      975      980      985
284 atc tca gcc ctc ctt cca gct gtg gcc cat ggg ggc aat tac ttc cta 3027
285 Ile Ser Ala Leu Leu Pro Ala Val Ala His Gly Gly Asn Tyr Phe Leu
286      990      995      1000
288 tca ctg tct caa gtc atc act aac aat gca agc tgc ata gtg cag aac 3075
289 Ser Leu Ser Gln Val Ile Thr Asn Asn Ala Ser Cys Ile Val Gln Asn
290      1005      1010      1015
292 ctg act gaa ccc cca ggc cca cct gtg cat cca gag gag ctt caa cac 3123
293 Leu Thr Glu Pro Pro Gly Pro Pro Val His Pro Glu Glu Leu Gln His
294      1020      1025      1030
296 aca aac aga ctg aat ggg agc aat act cag tgt cag gtg gtg agg tgc 3171
297 Thr Asn Arg Leu Asn Gly Ser Asn Thr Gln Cys Gln Val Val Arg Cys
298 1035      1040      1045      1050
300 cac ctt ggg cag ctg gca aag ggg act gag gtc tct gtt gga cta ttg 3219
301 His Leu Gly Gln Leu Ala Lys Gly Thr Glu Val Ser Val Gly Leu Leu
302      1055      1060      1065
304 agg ctg gtt cac aat gaa ttt ttc cga aga gcc aag ttc aag tcc ctg 3267
305 Arg Leu Val His Asn Glu Phe Phe Arg Arg Ala Lys Phe Lys Ser Leu
306      1070      1075      1080
308 acg gtg gtc agc acc ttt gag ctg gga acc gaa gag ggc agt gtc cta 3315
309 Thr Val Val Ser Thr Phe Glu Leu Gly Thr Glu Glu Gly Ser Val Leu
310      1085      1090      1095
312 cag ctg act gaa gcc tcc cgt tgg agt gag agc ctc ttg gag gtg gtt 3363
313 Gln Leu Thr Glu Ala Ser Arg Trp Ser Glu Ser Leu Leu Glu Val Val
314      1100      1105      1110
316 cag acc cgg cct atc ctc atc tcc ctg tgg atc ctc ata ggc agt gtc 3411
317 Gln Thr Arg Pro Ile Leu Ile Ser Leu Trp Ile Leu Ile Gly Ser Val
318 1115      1120      1125      1130
320 ctg gga ggg ttg ctc ctg ctt gct ctc ctt gtc ttc tgc ctg tgg aag 3459
321 Leu Gly Gly Leu Leu Leu Ala Leu Leu Val Phe Cys Leu Trp Lys
322      1135      1140      1145
324 ctt ggc ttc ttt gcc cat aag aaa atc cct gag gaa gaa aaa aga gaa 3507
325 Leu Gly Phe Phe Ala His Lys Lys Ile Pro Glu Glu Glu Lys Arg Glu

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Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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Input Set : A:\003300-685.ST25.txt

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L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15